# METHODS FOR LARGE SCALE PROTEIN MATCHING

## ABSTRACT OF THE DISCLOSURE

The present invention provides methods for matching a sample of an unknown query peptide to a database of known peptides. The methods described herein allow for the rapid, sensitive, and selective identification of an unknown query peptide, which enables the development of high throughput protein identification. The methods described herein also allow for mass spectrometry data for a query peptide to be categorized and weighted according to its quality. Furthermore, the methods described herein provide robust identification of modified query proteins by either anticipating modifications or adjusting for modified peptide masses.